

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2005, 17:05:58 ; Search time 176 Seconds
(without alignments)
75.648 Million cell updates/sec

Title: US-09-733-239-1

Perfect score: 139
Sequence: 1 RILAVERYLKDQQLGIWCGSGKLC 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	117	2 Q9YRU1	Q9YRU1 human immun
2	139	100.0	117	2 Q9YVZ9	Q9YVZ9 human immun
3	139	100.0	118	2 Q6WH32	Q6WH32 human immun
4	139	100.0	122	2 Q6DL09	Q6DL09 human immun
5	139	100.0	122	2 Q6DL62	Q6DL62 human immun
6	139	100.0	122	2 Q6WH41	Q6WH41 human immun
7	139	100.0	122	2 Q7ZJR4	Q7ZJR4 human immun
8	139	100.0	122	2 Q9EA97	Q9EA97 human immun
9	139	100.0	122	2 Q9QIU3	Q9QIU3 human immun
10	139	100.0	122	2 Q9WQZ3	Q9WQZ3 human immun
11	139	100.0	122	2 Q9YXPA	Q9YXPA human immun
12	139	100.0	123	2 Q8AEX2	Q8AEX2 human immun
13	139	100.0	134	2 Q698W3	Q698W3 human immun
14	139	100.0	144	2 Q7ZCD6	Q7ZCD6 human immun
15	139	100.0	145	2 Q7ZCD7	Q7ZCD7 human immun
16	139	100.0	145	2 Q7ZC48	Q7ZC48 human immun
17	139	100.0	145	2 Q7ZC52	Q7ZC52 human immun
18	139	100.0	147	2 Q6JFL9	Q6JFL9 human immun
19	139	100.0	155	2 Q8J3N1	Q8J3N1 human immun
20	139	100.0	357	2 Q78119	Q78119 human immun
21	139	100.0	358	2 Q78120	Q78120 human immun
22	139	100.0	588	2 Q933A7	Q933A7 human immun
23	139	100.0	588	2 Q933A8	Q933A8 human immun
24	139	100.0	589	2 Q933B1	Q933B1 human immun
25	139	100.0	590	2 Q933A9	Q933A9 human immun
26	139	100.0	616	2 Q933B0	Q933B0 human immun
27	139	100.0	618	2 Q933B2	Q933B2 human immun
28	139	100.0	727	2 Q90723	Q90723 human immun
29	139	100.0	746	2 Q6QLJ1	Q6QLJ1 human immun
30	139	100.0	746	2 Q6QLJ3	Q6QLJ3 human immun
31	139	100.0	747	2 Q70607	Q70607 human immun

32	139	100.0	748	2 Q70606	Q70606 human immun
33	139	100.0	752	2 Q70604	Q70604 human immun
34	139	100.0	752	2 Q70605	Q70605 human immun
35	139	100.0	752	2 Q70608	Q70608 human immun
36	139	100.0	757	2 Q9Q722	Q9Q722 human immun
37	139	100.0	768	2 Q6QLI8	Q6QLI8 human immun
38	139	100.0	800	2 Q9MMV1	Q9MMV1 human immun
39	139	100.0	801	2 Q9MMU9	Q9MMU9 human immun
40	139	100.0	807	2 Q8Q2X2	Q8Q2X2 human immun
41	139	100.0	809	2 Q6QLI5	Q6QLI5 human immun
42	139	100.0	809	2 Q9MMV0	Q9MMV0 human immun
43	139	100.0	826	2 Q9DVL1	Q9DVL1 human immun
44	139	100.0	845	2 Q6QEV1	Q6QEV1 human immun
45	139	100.0	845	2 Q9ID89	Q9ID89 human immun

ALIGNMENTS

RESULT 1
Q9YRU1 PRELIMINARY; PRT; 117 AA.
AC Q9YRU1;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DE 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=96USCM48;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Ial R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096324; AAD04399.1; -;
DR HSSP; Q88007; 1QBZ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR00328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 117
FT NON_TER 1 117
SQ SEQUENCE 117 AA; 13986 MW; 4719FD6EB98E42E3 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|||
Db 19 RILAVERYLKDQQLGIWCGSGKLC 44
|||

RESULT 2
Q9YVZ9 PRELIMINARY; PRT; 117 AA.
AC Q9YVZ9;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DE 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE GP41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=171.005;
RA Brennan C.A., Lund J.K., Golden A., Yanaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006876; AAD01320.1; -.
DR HSP; O91Q08; ICZL.
DR DR; GO:0016021; C:integral to membrane; IEA.
DR DR; GO:0019028; C:viral capsid; IEA.
DR DR; GO:0019031; C:viral envelope; IEA.
DR DR; GO:0005198; F:structural molecule activity; IEA.
DR DR; InterPro; IPR000328; Env_GP41.
DR DR; Pfam; PF00517; GP41; 1.
KW Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 13970 MW; 4B0F82FC9AF0756D CRC64;

Query Match 100.0%; Score 139; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 23 RILAVERYLKDQQLGIWGCSGKLC 48

RESULT 3
Q6WH32 PRELIMINARY; PRT; 118 AA.
ID Q6WH32
AC Q6WH32;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX PubMed=14715797;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations
RT and subtypes in drug-naïve, infected individuals in the army health
RT service of Rio de Janeiro, Brazil.";
RL J. Clin. Microbiol. 42:426-430(2004).
DR EMBL; AY285064; AAQ68127.1; -.
DR DR; GO:0016021; C:integral to membrane; IEA.
DR DR; GO:0019028; C:viral capsid; IEA.
DR DR; GO:0019031; C:viral envelope; IEA.
DR DR; GO:0005198; F:structural molecule activity; IEA.
DR DR; InterPro; IPR000328; Env_GP41.
DR DR; Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14303 MW; FC6437BD5749A4B8 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 15 RILAVERYLKDQQLGIWGCSGKLC 40

RESULT 4
Q6DL09 PRELIMINARY; PRT; 122 AA.
ID Q6DL09
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AC Q6DL09;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,
RA Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,
RA Folks T.M.;
RT "Recombinant viruses and early global HIV-1 epidemic.";
RL Emerg. Infect. Dis. 10:1227-1234(2004).
DR EMBL; AY667694; AAT75000.1; -.
DR DR; GO:0019031; C:viral envelope; IEA.
DR DR; GO:0005198; F:structural molecule activity; IEA.
DR DR; InterPro; IPR000328; Env_GP41.
DR DR; Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14712 MW; 9D69569A666BD069 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLC 44

RESULT 5
Q6DL62 PRELIMINARY; PRT; 122 AA.
ID Q6DL62
AC Q6DL62;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,
RA Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,
RA Folks T.M.;
RT "Recombinant viruses and early global HIV-1 epidemic.";
RL Emerg. Infect. Dis. 10:1227-1234(2004).
DR EMBL; AY667694; AAT74947.1; -.
DR DR; GO:0019031; C:viral envelope; IEA.
DR DR; GO:0005198; F:structural molecule activity; IEA.
DR DR; InterPro; IPR000328; Env_GP41.
DR DR; Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14692 MW; 60291A1AEE96713C CRC64;

Query Match 100.0%; Score 139; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLC 44
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RESULT 6
Q6WH41 ID Q6WH41 PRELIMINARY; PRT; 122 AA.
AC Q6WH41;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14715797;
RA Pires I.L., Soares M.A., Speranza F.A.B., Iehli S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations
RT and subtypes in drug-naïve, infected individuals in the army health
RT service of Rio de Janeiro, Brazil.";
RL J. Clin. Microbiol. 42:426-430(2004).
DR EMBL; AY285055; AAQ68118.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT SEQUENCE 122 AA; 14817 MW; FEF95657A2C81ACC CRC64;
L Query Match 100.0%; Score 139; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 19 RILAVERYLKDQQLGIGCSGKLC 44

RESULT 7
Q7ZJR4 ID Q7ZJR4 PRELIMINARY; PRT; 122 AA.
AC Q7ZJR4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22800244; PubMed=12921095; DOI=10.1089/08922203322231003;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL AIDS Res. Hum. Retroviruses 19:625-629(2003).
DR EMBL; AY214095; AAQ61815.1; -.
DR HSP; P12488; 11W7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 122
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FT NON_TER 122
SQ SEQUENCE 122 AA; 14777 MW; AE2C9F40DF21CCFB CRC64;
L Query Match 100.0%; Score 139; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 19 RILAVERYLKDQQLGIGCSGKLC 44

RESULT 8
Q9EA97 ID Q9EA97 PRELIMINARY; PRT; 122 AA.
AC Q9EA97;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190955; AAG02317.1; -.
DR HSP; P12488; 11W7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT SEQUENCE 122 AA; 14763 MW; B9207B0EBE4213AA CRC64;
L Query Match 100.0%; Score 139; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 19 RILAVERYLKDQQLGIGCSGKLC 44

RESULT 9
Q9QIU3 ID Q9QIU3 PRELIMINARY; PRT; 122 AA.
AC Q9QIU3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580799; PubMed=11724274; DOI=10.1023/A:1011812810397;
RA Caride E., Hertogh K., Larder B., Denertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer-Silva W.A., Slon F.S., Passioni L.F.C.,
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RA Menezes J.A., Calazans A.R., Tanuri A.;
 RT "Genotypic and phenotypic evidence of different drug-resistance
 RT mutation patterns between B and non-B subtype isolates of human
 RT immunodeficiency virus type 1 found in Brazilian patients failing
 RT HAART.";
 RL Virus Genes 23:193-202(2001).
 DR EMBL; AF165561; AAP08506.1; --
 DR HSP; P12488; 1M7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14817 MW; 8D6099E5D3993205 CRC64;

 Query Match 100.0%; Score 139; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RILAVERYLKDQQLGWCCKLIC 26
 |||||
 DB 19 RILAVERYLKDQQLGWCCKLIC 44

 RESULT 10
 Q9WQZ3
 ID Q9WQZ3 PRELIMINARY; PRT; 122 AA.
 AC Q9WQZ3;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Names=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1] (Fragment).
 RP SEQUENCE FROM N.A.
 RA Pieniazek D., Yang C., Lal R.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF113589; AAD42757.1; --
 DR HSP; Q91J08; 1GZL.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14703 MW; 09E2E31B37786D34 CRC64;

 Query Match 100.0%; Score 139; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RILAVERYLKDQQLGWCCKLIC 26
 |||||
 DB 19 RILAVERYLKDQQLGWCCKLIC 44

 RESULT 11
 Q9YXP4
 ID Q9YXP4 PRELIMINARY; PRT; 122 AA.
 AC Q9YXP4;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Envelope glycoprotein immunodominant region (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1] (Fragment).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99125811; PubMed=9928731;
 RA Tanuri A., Swanson P., Devare S., Berro O.J., Savedra A., Costa L.J.,
 RA Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.,
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
 RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 20:60-66(1999).
 DR EMBL; AF034059; AAC79311.1; --
 DR HSP; Q91J08; 1GZL.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14819 MW; E3960B97ED1C08D6 CRC64;

 Query Match 100.0%; Score 139; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RILAVERYLKDQQLGWCCKLIC 26
 |||||
 DB 19 RILAVERYLKDQQLGWCCKLIC 44

 RESULT 12
 Q9AEX2
 ID Q9AEX2 PRELIMINARY; PRT; 123 AA.
 AC Q9AEX2;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Gp41 (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1] (Fragment).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22771871; PubMed=12892060; DOI=10.1089/08922203766774568;
 RA Esteves A., Parreira R., Piedade J., Venenno T., Franco M.,
 RA Germano De Sousa J., Patricia L., Brum P., Costa A.,
 RA Canas-Ferreira W.F.;
 RT "Spreading of HIV-1 subtype G and envB/gag recombinant strains among
 RT injecting drug users in Lisbon, Portugal."
 RL AIDS Res. Hum. Retroviruses 19:511-517(2003).
 DR EMBL; AJ429041; CAD23677.1; --
 DR HSP; P04624; 1JAU.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 14895 MW; 489C41C5C275D88F CRC64;

 Query Match 100.0%; Score 139; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RILAVERYLKDQQLGWCCKLIC 26

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FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EEB CRC64;

Query Match 100.0%; Score 139; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY * 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 50 RILAVERYLKDQQLLGWCSGKLIC 75

RESULT 15
Q7ZCD7 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX MEDLINE=22679027; PubMed=12794544;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1 strains.";
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY185383; AAO65658.1; -.
DR HSP; P04578; IAIK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318EBE CRC64;

Query Match 100.0%; Score 139; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 50 RILAVERYLKDQQLLGWCSGKLIC 75

Search completed: March 3, 2005, 17:22:15
Job time : 178 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2005, 17:13:03 ; Search time 39 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-09-733-239-1

Perfect score: 139

Sequence: 1 RILAVERYLKDQQLGIGWCSGKLLC 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	357	2 S21996	envelope protein g
2	139	100.0	358	2 S21998	envelope protein g
3	139	100.0	853	2 S54384	envelope polyprote
4	139	100.0	854	2 S13288	env protein - huma
5	139	100.0	855	1 VCLJZR	env polyprotein pr
6	139	100.0	856	1 VCLJH3	env polyprotein pr
7	139	100.0	856	1 VCLJVL	env polyprotein pr
8	139	100.0	861	1 VCLJLV	env polyprotein g
9	138	99.3	357	2 S22004	envelope protein g
10	138	99.3	357	2 S22006	envelope protein g
11	138	99.3	357	2 S21992	envelope protein g
12	138	99.3	357	2 S21994	envelope protein g
13	138	99.3	852	1 VCLJBR	env polyprotein -
14	137	98.6	856	1 A44963	env polyprotein pr
15	135	97.1	357	2 S21990	envelope protein g
16	135	97.1	358	2 S70417	envelope protein g
17	135	97.1	358	2 S22000	envelope protein g
18	135	97.1	358	2 S22002	envelope protein g
19	135	97.1	443	2 C41621	env polyprotein p
20	135	97.1	445	2 B41621	env polyprotein M
21	135	97.1	454	2 B41621	env polyprotein D
22	135	97.1	843	1 H44001	env polyprotein pr
23	135	97.1	852	2 T12016	envelope glycoprot
24	135	97.1	855	1 VCLJAJ	env polyprotein pr
25	135	97.1	856	1 VCLJ3W	env polyprotein pr
26	135	97.1	861	1 VCLJSC	env polyprotein pr
27	135	97.1	868	1 VCLJH4	env polyprotein -
28	134	96.4	859	1 VCLJMN	env polyprotein pr
29	132	95.0	729	1 VCLJFK	env polyprotein pr

30 132 95.0 851 2 S33985 env polyprotein -
31 132 95.0 861 1 VCLJKB env polyprotein pr
32 131 94.2 847 2 T09448 envelope glycoprot
33 131 94.2 847 2 S13289 env protein - huma
34 125 89.9 846 1 VCLJND env polyprotein pr
35 123 88.5 854 1 VCLJSI env polyprotein pr
36 120 86.3 859 2 T01672 envelope polyprote
37 98 70.5 863 2 AS3034 gag polyprotein -
38 92 66.2 877 2 S49197 envelope protein p
39 91 65.5 104 2 S52930 GP41 ENV protein -
40 89 64.0 855 2 A45713 Env transmembrane
41 86 61.9 859 1 VCLJST env polyprotein pr
42 84 60.4 869 2 A47665 env protein gp120(
43 84 60.4 881 2 S03068 env protein - huma
44 83 59.7 151 2 S30453 env protein - huma
45 83 59.7 151 2 S30451 env protein - huma

ALIGNMENTS

RESULT 1

S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78119; EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G10671;
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGWCSGKLLC 26

Db 80 RILAVERYLKDQQLGIGWCSGKLLC 105

RESULT 2

S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STEL>
A:Cross-references: UNIPROT:Q78120; EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-55, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 81 RILAVERYLKDQQLGIWGCGSKLIC 106
|||||

RESULT 3

S54384

envelope polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-853 <THE>

A:Cross-references: UNIPROT:P12487; EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g3293

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: polyprotein

Query Match 100.0%; Score 139; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 576 RILAVERYLKDQQLGIWGCGSKLIC 601
|||||

RESULT 4

S13288

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q78243; UNIP

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 577 RILAVERYLKDQQLGIWGCGSKLIC 602
|||||

RESULT 5

VCLJZR

env polyprotein precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus Zr-6

C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: D26192

R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti

A:Reference number: A26192; MUID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: UNIPROT:P04580; GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; I

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-855/Product: env polyprotein #status predicted <MAT>

F:501-855/Product: exterior membrane glycoprotein #status predicted <EXT>

F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 100.0%; Score 139; DB 1; Length 855;

Best Local Similarity 100.0%; Pred. No. 5.4e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||

DB 578 RILAVERYLKDQQLGIWGCGSKLIC 603
|||||

RESULT 6

VCLJH3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar

nberger, J.A.; Papas, T.S.; Chrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; MUID:85111123; PMID:2578615

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>

A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326;

C:Genetics:

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>

F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,

F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 100.0%; Score 139; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No. 5.4e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||

DB 579 RILAVERYLKDQQLGIWGCGSKLIC 604
|||||

RESULT 7

VCLJVL

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03974

R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.

Nature 313, 450-458, 1985

A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovir

A:Reference number: A93355; MUID:85111157; PMID:2982104

A:Accession: A03974

A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: UNIPROT:P03376; GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88-136.141.156.160.196.197.230.234.241.262.276.289.295.301.332.339.356.386.392.397.406
F:611.616.625.637.674.750.816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 579 RILAVERYLKDQQLGIGWCSGKLC 604
RESULT 8
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAI>
A:Cross-references: UNIPROT:P03377; GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMM>
F:88-136.141.146.161.165.191.202.239.246.267.281.294.300.306.337.344.361.391.397.402.411
F:616.621.630.642.679.755.821/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 139; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 584 RILAVERYLKDQQLGIGWCSGKLC 609
RESULT 9
S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 4B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: UNIPROT:Q78155; EMBL:X61353; NID:G60188; PIDN:CAA43618.1; PID:G60189
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70419
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-292, 'X', 294-357 <STE2>
A:Cross-references: EMBL:X61353; NID:G60188
C:Superfamily: type E retrovirus env polyprotein
Query Match 99.3%; Score 138; DB 2; Length 357;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGWCSGKLC 105
RESULT 10
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70420
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78156; EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191
A:Experimental source: patient L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein
Query Match 99.3%; Score 138; DB 2; Length 357;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGWCSGKLC 105
RESULT 11
S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70424; S21992
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70424
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78112; EMBL:X61358; NID:G60177; PIDN:CAA43628.1; PID:G60178
A:Experimental source: patient 22
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein
Query Match 99.3%; Score 138; DB 2; Length 357;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGWCSGKLC 105

RESULT 12

S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: UNIPROT:Q78118; EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:G60179
C:Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 1; Length 357;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 80 RVLAVERYLKDQQLGIWCGSGKLC 105
|:|||||

RESULT 13

VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31667
R:Anand, R.; Thayer, R.; Srinivasaan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1) isolates
A:Reference number: A94389; MUID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
A:Cross-references: UNIPROT:P12498
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 99.3%; Score 138; DB 1; Length 852;
Best Local Similarity 96.2%; Pred. No. 7.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 575 RVLAVERYLKDQQLGIWCGSGKLC 600
|:|||||

RESULT 14

A44963
env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A44963
R:Srinivasaan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence
A:Reference number: A44963; MUID:89228766; PMID:2713163
A:Accession: A44963
A:Molecule type: DNA
A:Residues: 1-856 <SRI>
A:Cross-references: UNIPROT:P05881; GB:M15896; NID:G329392; PIDN:AAB53948.1; PID:G329394
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-520/Product: coat protein gp120 #status predicted <CP1>
F:521-856/Product: coat protein gp41 #status predicted <CP2>
F:584-705/Domain: transmembrane #status predicted <TMN>
F:87,132,138,152,156,183,198,242,263,277,294,302,339,398,402,411,448,461,462,465,611,
Query Match 98.6%; Score 137; DB 1; Length 856;
Best Local Similarity 96.2%; Pred. No. 1.1e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 579 RILAVERYLKDQQLGIWCGSGKLC 604
|:|||||

RESULT 15

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 20
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21990; S70423
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: UNIPROT:Q78100; EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176
C:Superfamily: type E retrovirus env polyprotein

Query Match 97.1%; Score 135; DB 2; Length 357;
Best Local Similarity 92.3%; Pred. No. 9e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 80 RVLAVERYLKDQQLGIWCGSGKLC 105
|:|||||

Search completed: March 3, 2005, 17:22:58
Job time : 39 secs